

5'	GC	CGC	TGC	CAC	GCC	CTT	GGG	CCG	CCG	CGC	GCC	GGC	GCC	TCT	TCC	TTC	CGC	TTG	54
	63	TGT	GAG	CTG	AGG	CGG	TGT	ATG	TGC	GGC	AAT	AAC	ATG	TCA	ACC	CCG	CTG	CCC	108
							M	C	G	N	N	N	M	S	T	P	L	P	
	117	ATC	GTG	CCC	GCC	GCC	CGG	AAG	GCC	ACC	GCT	GCG	GTG	ATT	TTC	CTG	CAT	GGA	162
		A	I	V	P	A	A	R	K	A	T	A	V	I	F	L	H	G	
	171	GGA	GAT	ACT	GGG	CCT	GTT	AGG	CCT	GTT	ACA	TTA	AAT	ATG	AAC	GTG	GCT	ATG	216
		L	G	D	T	G	P	V	R	P	V	T	L	N	M	N	V	A	M
	225	TCA	TGG	TTT	GAT	ATT	ATT	GGG	CTT	TCA	CCA	GAT	TCA	CAG	GAG	GAT	GAA	TCT	270
		P	S	W	F	D	I	I	G	L	S	P	D	S	Q	E	D	E	S
	279	ATT	AAA	CAG	GCA	GCA	GAA	AAT	ATA	AAA	GCT	TTG	ATT	GAT	CAG	GAA	GTG	AAG	324
		G	I	K	Q	A	A	E	N	I	K	A	L	I	D	O	E	V	K

FIGURE 1A

333	342	351	360	369	378
AAT GGC ATT CCT TCT AAC AGA ATT ATT TTG GGA GGG TTT TCT CAG GGA GGT					
N G I P S N R I I L G G F S Q G G A					
387	396	405	414	423	432
TTA TCT TTA TAT ACT GCC CTT ACC ACA CAG CAG AAA CTG GCA GGT GTC ACT GCA					
L S L Y T A L T T Q Q K L A G V T A					
441	450	459	468	477	486
CTC AGT TTC TTG CTT CCA CTT CGG GNT TCC TTT CCA CAG GKG CCT ATC GGT GGT					
L S F L L P L L R X S F P Q G P I G G					
495	504	513	522	531	540
GCT AAT AGA GAT ATT TCT ATT CTC CAG TGC CAC GGG GAT TGT GAC CCT TTG GTT					
A N R D I S I L Q C H G D C D P L V					
549	558	567	576	585	594
CCC CTG ATG TTT GGT TCT CTT ACG GTG GAA AAA CTA AAA ACA TTG GTG AAT CCA					
P L M F G S L T V E K L K T L V N P					
603	612	621	630	639	648
GCC AAT GTG ACC TTT AAA ACC TAT GAA GGT ATG CAC AGT TCG TGT CAA CAG					
A N V T F K K T Y E G M M H S S C Q					

FIGURE 1B

657	GAA	ATG	ATG	GAT	GTC	AAG	CAA	TTC	ATT	GAT	AAA	CTC	CTA	CCT	CCA	ATT	GAT	TGA	702
	E	M	M	D	V	K	Q	F	I	D	K	L	L	P	P	I	D		
	CGT CAC TA 3'																		
	R	H																	

FIGURE 1C

1 MCGNNMSTPLPAIVPAARKATAAIVFLHGLGDTG-- -- -- -- 2676650
1 MCGNNMS[A][M]PA[V]VPAARKATAAIVFLHGLGDTG[H][G][W][A][E][A] GI 1552244

35 --
41 F A G I K S S H I K Y I C P H A P V [M] P V T L N M [S][M] M P S W F D I I G L S P 2676650
GI 1552244

59 D S Q E D E S G I K Q A A E N I K A L I D Q E V K N G I P S N R I I L G G F S Q 2676650
81 D S Q E D E S G I K Q A A E [T][V] K A L I D Q E V K N G I P S N R I I L G G F S Q GI 1552244

99 G G A L S L Y T A L T T Q Q K L A G V T A L S F L L P L R [X] S F P Q G P I G G A 2676650
121 G G A L S L Y T A L T T Q Q K L A G V T A L S [C][W] L P L R A S F [S] Q G P I [N][S] A GI 1552244

139 N R D I S I L Q C H G D C D P L V P L M F G S L T V E K L K T L V N P A N V T F 2676650
161 N R D I S [V] L Q C H G D C D P L V P L M F G S L T V E [R] L K [G] L V N P A N V T F GI 1552244

179 K T Y E G M M H S S C Q Q E M M D V K Q F I D K L L P P I D 2676650
201 K [V] Y E G M M H S S C Q Q E M M D V K [Y] F I D K L L P P I D GI 1552244

FIGURE 2

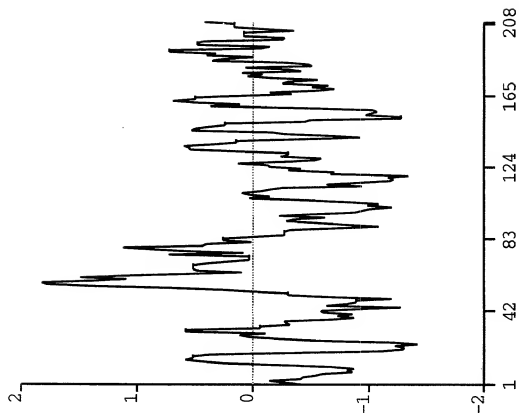


FIGURE 3A

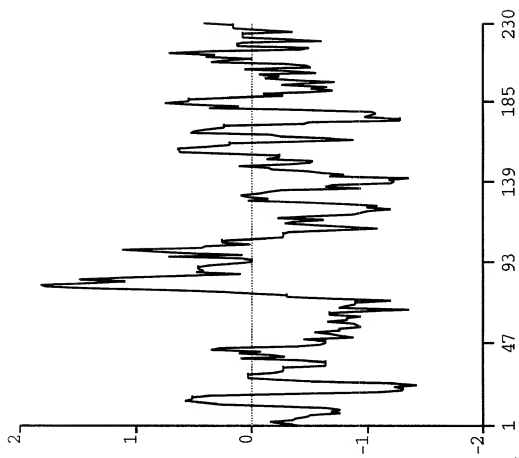


FIGURE 3B

Library	Lib Description	Abun	Pct Abun
U937NOT01	U937 monocyte cell line, 37 M	3	0.1491
COCHFEM01	ear, cochlea, fetal, WM	1	0.1157
RATRNOT01	heart, right atrium, 51 F	1	0.0874
OVARUT04	ovarian tumor, 53 F	3	0.0755
TBLYNOT01	T-B lymphoblast cell line, leukemia	2	0.0652
PGANNCOT03	paraganglionic tumor, benign paraganglioma, 46 M	2	0.0622
ENDNCOT01	endothelial cells, coronary artery, 58 M	2	0.0535
MPHGCNOT03	macrophages (adher PBMC), M/F	4	0.0517
FIBRNOT01	WI38 lung fibroblast cell line, 3m F	1	0.0469
ADENINB01	adenoid, inflamed, 3y	2	0.0381
BLADNOT01	bladder, 78 F	1	0.0350
COLNNOT05	colon, 40 M, match to COLNCR01	1	0.0289
UTRSNOT06	uterus, myometrium, 50 F	1	0.0282
BLADTUT07	bladder, microfoci tumor, 58 M	1	0.0278
HYPONOB01	hypothalamus, 16-75 M/F	1	0.0272
PROSNOT16	prostate, 68 M	2	0.0263
KIDNNOT19	kidney, 65 M	1	0.0259
COLNTUT16	colon tumor, 60 M, match to COLNNOT07/08/09/11	1	0.0256
THYRNOT09	thyroid, adenomatous goiter, 18 F	1	0.0254
HNT2AGT01	hNT2 cell line, post-mitotic neurons	1	0.0192
HNT3AZT01	hNT2 cell line, teratocarcinoma, treated AZ	1	0.0191
HNT2NOT01	hNT2 cell line, teratocarcinoma, untreated	1	0.0173
SINTBST01	small intestine, ileum, Crohn's, 18 F	1	0.0168
BEPINOT01	bronchial epithelium, primary cell line, 54 M	1	0.0144
BRSTTUT02	breast tumor, 54 F, match to BRSTNOT03	1	0.0140

FIGURE 4A

TESTTUT02	testicular tumor, 31 M	1	0.0134
CONUTUT01	mesenteric tumor, sigmoid, 61 F	1	0.0130
SINTFET03	small intestine, fetal F	1	0.0130
THPINOT03	THP-1 promonocyte cell line, untreated	1	0.0129
PROSTUT04	prostate tumor, 57 M, match to PROSNOT06	1	0.0117
PLACNOM02	placenta, neonatal F, NORM, WM	2	0.0111
BRSTNOT04	breast, 62 F	1	0.0096
PROSNOM01	prostate, 28 M, NORM	1	0.0094
BRAINOM01	brain, infant F, NORM, WM	2	0.0089
PANCTUT02	pancreatic tumor, carcinoma, 45 F	1	0.0086
LUNGFET03	lung, fetal F	1	0.0069

FIGURE 4B